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RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/226,046

DATE: 08/06/1999  
TIME: 15:41:04

Input Set: I226046.RAW

This Raw Listing contains the General Information  
Section and up to first 5 pages.

ENTERED

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1  <110> APPLICANT: Reppert, Steven M.
2      Ebisawa, Takashi
3  <120> TITLE OF INVENTION: HIGH-AFFINITY MELATONIN RECEPTOR AND USES THEREOF
4  <130> FILE REFERENCE: 10217/250003
5  <140> CURRENT APPLICATION NUMBER: US/09/226,046
6  <141> CURRENT FILING DATE: 1999-01-05
7  <150> EARLIER APPLICATION NUMBER: US 08/466,103
8  <151> EARLIER FILING DATE: 1995-06-06
9  <150> EARLIER APPLICATION NUMBER: US 08/319,887
10 <151> EARLIER FILING DATE: 1994-10-07
11 <150> EARLIER APPLICATION NUMBER: US 08/261,857
12 <151> EARLIER FILING DATE: 1994-06-17
13 <160> NUMBER OF SEQ ID NOS: 29
14 <170> SOFTWARE: FastSEQ for Windows Version 3.0
15 <210> SEQ ID NO 1
16 <211> LENGTH: 1320
17 <212> TYPE: DNA
18 <213> ORGANISM: Xenopus laevis
19 <220> FEATURE:
20 <221> NAME/KEY: CDS
21 <222> LOCATION: (32)...(1291)
22 <400> SEQUENCE: 1
23      tgcctatctc cctttgccag ggggcagaga a atg atg gag gtg aat agc act      52
24                                     Met Met Glu Val Asn Ser Thr
25                                     1           5
26      tgc ttg gat tgc agg aca cct ggt acc ata cga aca gag cag gat gca      100
27      Cys Leu Asp Cys Arg Thr Pro Gly Thr Ile Arg Thr Glu Gln Asp Ala
28          10           15           20
29      cag gac agc gca tct cag gga ctc acc tct gcc ctg gcg gtg gtt ctt      148
30      Gln Asp Ser Ala Ser Gln Gly Leu Thr Ser Ala Leu Ala Val Val Leu
31          25           30           35
32      ata ttc acc att gtt gtg gat gtc ctg ggc aat ata ttg gtc att ttg      196
33      Ile Phe Thr Ile Val Val Asp Val Leu Gly Asn Ile Leu Val Ile Leu
34          40           45           50           55
35      tct gtc ctg agg aac aag aag ctg cag aat gct gga aat ctc ttt gtt      244
36      Ser Val Leu Arg Asn Lys Lys Leu Gln Asn Ala Gly Asn Leu Phe Val
37          60           65           70
38      gtc agt ttg tct att gcc gat ctg gtt gtt gct gtg tat ccc tat ccg      292
39      Val Ser Leu Ser Ile Ala Asp Leu Val Val Ala Val Tyr Pro Tyr Pro
40          75           80           85
41      gtc att ctc ata gct att ttc cag aat gga tgg acg ctt gga aat atc      340
42      Val Ile Leu Ile Ala Ile Phe Gln Asn Gly Trp Thr Leu Gly Asn Ile
43          90           95           100
44      cat tgt cag atc agt ggc ttc ctg atg gga ctc agc gtt att gga tca      388

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45	His Cys Gln Ile Ser Gly Phe Leu Met Gly Leu Ser Val Ile Gly Ser	
46	105 110 115	
47	gtc ttc aac ata aca gcc ata gct atc aac agg tat tgc tac atc tgc	436
48	Val Phe Asn Ile Thr Ala Ile Ala Ile Asn Arg Tyr Cys Tyr Ile Cys	
49	120 125 130 135	
50	cac agc ctg aga tat gac aag ctt tat aat caa aga agc acc tgg tgc	484
51	His Ser Leu Arg Tyr Asp Lys Leu Tyr Asn Gln Arg Ser Thr Trp Cys	
52	140 145 150	
53	tac ctt ggc ctg aca tgg ata cta act ata att gca atc gtg cca aac	532
54	Tyr Leu Gly Leu Thr Trp Ile Leu Thr Ile Ile Ala Ile Val Pro Asn	
55	155 160 165	
56	ttt ttt gtt gga tca cta cag tat gac ccc agg att ttt tct tgc aca	580
57	Phe Phe Val Gly Ser Leu Gln Tyr Asp Pro Arg Ile Phe Ser Cys Thr	
58	170 175 180	
59	ttt gcg cag aca gtg agt tcc tca tac acc ata aca gta gtg gtg gtg	628
60	Phe Ala Gln Thr Val Ser Ser Ser Tyr Thr Ile Thr Val Val Val Val	
61	185 190 195	
62	cat ttt ata gtc cct ctt agt gtt gtg aca ttc tgt tac tta aga ata	676
63	His Phe Ile Val Pro Leu Ser Val Val Thr Phe Cys Tyr Leu Arg Ile	
64	200 205 210 215	
65	tgg gtt tta gtg atc caa gtc aaa cac aga gtt aga caa gac ttc aag	724
66	Trp Val Leu Val Ile Gln Val Lys His Arg Val Arg Gln Asp Phe Lys	
67	220 225 230	
68	caa aag ttg aca caa aca gac ttg aga aat ttc ttg acc atg ttt gtg	772
69	Gln Lys Leu Thr Gln Thr Asp Leu Arg Asn Phe Leu Thr Met Phe Val	
70	235 240 245	
71	gtc ttt gta ctt ttt gca gtt tgc tgg gcc ccc tta aac ttt atc ggc	820
72	Val Phe Val Leu Phe Ala Val Cys Trp Ala Pro Leu Asn Phe Ile Gly	
73	250 255 260	
74	ctt gct gtg gcc att aat ccg ttt cat gtg gca cca aag att cca gaa	868
75	Leu Ala Val Ala Ile Asn Pro Phe His Val Ala Pro Lys Ile Pro Glu	
76	265 270 275	
77	tgg ctg ttt gtt tta agc tat ttc atg gcc tat ttt aac agt tgt ctc	916
78	Trp Leu Phe Val Leu Ser Tyr Phe Met Ala Tyr Phe Asn Ser Cys Leu	
79	280 285 290 295	
80	aat gct gtt ata tat ggt gtg cta aat caa aac ttc cgc aag gag tac	964
81	Asn Ala Val Ile Tyr Gly Val Leu Asn Gln Asn Phe Arg Lys Glu Tyr	
82	300 305 310	
83	aaa aga ata ctg atg tcc tta ttg act cca aga ctg ttg ttt ctt gac	1012
84	Lys Arg Ile Leu Met Ser Leu Leu Thr Pro Arg Leu Leu Phe Leu Asp	
85	315 320 325	
86	aca tct aga gga gga act gag gga ttg aaa agt aag cct tcg cca gct	1060
87	Thr Ser Arg Gly Gly Thr Glu Gly Leu Lys Ser Lys Pro Ser Pro Ala	
88	330 335 340	
89	gta acc aac aac aat caa gca gat atg cta gga gaa gca agg tca ctg	1108
90	Val Thr Asn Asn Asn Gln Ala Asp Met Leu Gly Glu Ala Arg Ser Leu	
91	345 350 355	
92	tgg ctg agc agg aga aat ggt gcg aaa atg gtg atc atc atc agg cca	1156
93	Trp Leu Ser Arg Arg Asn Gly Ala Lys Met Val Ile Ile Ile Arg Pro	
94	360 365 370 375	

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95      aga aaa gca caa att gca atc atc cat caa ata ttc tgg cct cag agt      1204
96      Arg Lys Ala Gln Ile Ala Ile Ile His Gln Ile Phe Trp Pro Gln Ser
97              380                      385                      390
98      tca tgg gca aca tgc cgt caa gac aca aag att acc gga gaa gaa gat      1252
99      Ser Trp Ala Thr Cys Arg Gln Asp Thr Lys Ile Thr Gly Glu Glu Asp
100              395                      400                      405
101      ggc tgc cgt gaa ctg tgc aag gac ggg att tcc caa agg tgagacccaa      1301
102      Gly Cys Arg Glu Leu Cys Lys Asp Gly Ile Ser Gln Arg
103              410                      415                      420
104      tgcactatat ccacattat      1320
105      <210> SEQ ID NO 2
106      <211> LENGTH: 420
107      <212> TYPE: PRT
108      <213> ORGANISM: Xenopus laevis
109      <400> SEQUENCE: 2
110      Met Met Glu Val Asn Ser Thr Cys Leu Asp Cys Arg Thr Pro Gly Thr
111              1              5              10              15
112      Ile Arg Thr Glu Gln Asp Ala Gln Asp Ser Ala Ser Gln Gly Leu Thr
113              20              25              30
114      Ser Ala Leu Ala Val Val Leu Ile Phe Thr Ile Val Val Asp Val Leu
115              35              40              45
116      Gly Asn Ile Leu Val Ile Leu Ser Val Leu Arg Asn Lys Lys Leu Gln
117              50              55              60
118      Asn Ala Gly Asn Leu Phe Val Val Ser Leu Ser Ile Ala Asp Leu Val
119              65              70              75              80
120      Val Ala Val Tyr Pro Tyr Pro Val Ile Leu Ile Ala Ile Phe Gln Asn
121              85              90              95
122      Gly Trp Thr Leu Gly Asn Ile His Cys Gln Ile Ser Gly Phe Leu Met
123              100             105             110
124      Gly Leu Ser Val Ile Gly Ser Val Phe Asn Ile Thr Ala Ile Ala Ile
125              115             120             125
126      Asn Arg Tyr Cys Tyr Ile Cys His Ser Leu Arg Tyr Asp Lys Leu Tyr
127              130             135             140
128      Asn Gln Arg Ser Thr Trp Cys Tyr Leu Gly Leu Thr Trp Ile Leu Thr
129              145             150             155             160
130      Ile Ile Ala Ile Val Pro Asn Phe Phe Val Gly Ser Leu Gln Tyr Asp
131              165             170             175
132      Pro Arg Ile Phe Ser Cys Thr Phe Ala Gln Thr Val Ser Ser Ser Tyr
133              180             185             190
134      Thr Ile Thr Val Val Val Val His Phe Ile Val Pro Leu Ser Val Val
135              195             200             205
136      Thr Phe Cys Tyr Leu Arg Ile Trp Val Leu Val Ile Gln Val Lys His
137              210             215             220
138      Arg Val Arg Gln Asp Phe Lys Gln Lys Leu Thr Gln Thr Asp Leu Arg
139              225             230             235             240
140      Asn Phe Leu Thr Met Phe Val Val Phe Val Leu Phe Ala Val Cys Trp
141              245             250             255
142      Ala Pro Leu Asn Phe Ile Gly Leu Ala Val Ala Ile Asn Pro Phe His
143              260             265             270
144      Val Ala Pro Lys Ile Pro Glu Trp Leu Phe Val Leu Ser Tyr Phe Met

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145		275		280		285		
146	Ala	Tyr	Phe	Asn	Ser	Cys	Leu	Asn
147		290		295		300		
148	Gln	Asn	Phe	Arg	Lys	Glu	Tyr	Lys
149		305		310		315		320
150	Pro	Arg	Leu	Leu	Phe	Leu	Asp	Thr
151			325		330		335	
152	Lys	Ser	Lys	Pro	Ser	Pro	Ala	Val
153			340		345		350	
154	Leu	Gly	Glu	Ala	Arg	Ser	Leu	Trp
155		355		360		365		
156	Met	Val	Ile	Ile	Ile	Arg	Pro	Arg
157		370		375		380		
158	Gln	Ile	Phe	Trp	Pro	Gln	Ser	Ser
159		385		390		395		400
160	Lys	Ile	Thr	Gly	Glu	Glu	Asp	Gly
161			405		410		415	
162	Ile	Ser	Gln	Arg				
163			420					
164	<210>	SEQ ID NO 3						
165	<211>	LENGTH: 1149						
166	<212>	TYPE: DNA						
167	<213>	ORGANISM: Ovis						
168	<220>	FEATURE:						
169	<221>	NAME/KEY: CDS						
170	<222>	LOCATION: (49)...(1146)						
171	<400>	SEQUENCE: 3						
172	gggagctcga	cgctctgggg	atccaccggc	gccggccctg	ccagcgcg	atg	gcg	ggg
173							Met	Ala
174								Gly
175	cg	ctg	tgg	ggc	tcg	ccg	ggc	ggg
176	Arg	Leu	Trp	Gly	Ser	Pro	Gly	Gly
177		5		10		15		
178	gcg	ctg	ctc	aac	gtc	tcg	cag	gcg
179	Ala	Leu	Leu	Asn	Val	Ser	Gln	Ala
180		20		25		30		35
181	cg	ccg	cg	ccc	tcg	tgg	ctg	gcc
182	Arg	Pro	Arg	Pro	Ser	Trp	Leu	Ala
183			40		45		50	
184	ttc	acc	atc	gtg	gtg	gac	atc	gtg
185	Phe	Thr	Ile	Val	Val	Asp	Ile	Val
186		55		60		65		
187	gtg	tat	cgg	aac	aag	aag	ctg	agg
188	Val	Tyr	Arg	Asn	Lys	Lys	Leu	Arg
189		70		75		80		
190	agc	ctg	gca	gtt	gca	gac	ctg	ctg
191	Ser	Leu	Ala	Val	Ala	Asp	Leu	Leu
192		85		90		95		
193	gcg	ctg	gcg	tct	ata	gtt	aac	aat
194	Ala	Leu	Ala	Ser	Ile	Val	Asn	Asn

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**RAW SEQUENCE LISTING**  
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195	100	105	110	115	
196	tgc caa ctt agt ggc ttc ctg atg ggc ttg agc gtc atc ggg tcc gtt				441
197	Cys Gln Leu Ser Gly Phe Leu Met Gly Leu Ser Val Ile Gly Ser Val				
198		120	125	130	
199	ttc agc atc acg gga att gcc atc aac cgc tat tgc tgc atc tgc cac				489
200	Phe Ser Ile Thr Gly Ile Ala Ile Asn Arg Tyr Cys Cys Ile Cys His				
201		135	140	145	
202	agc ctc aga tac ggc aag ctg tat agc ggc acg aat tcc ctc tgc tac				537
203	Ser Leu Arg Tyr Gly Lys Leu Tyr Ser Gly Thr Asn Ser Leu Cys Tyr				
204		150	155	160	
205	gtg ttc ctg atc tgg acg ctg acg ctc gtg gcg atc gtg ccc aac ctg				585
206	Val Phe Leu Ile Trp Thr Leu Thr Leu Val Ala Ile Val Pro Asn Leu				
207		165	170	175	
208	tgt gtg ggg acc ctg cag tac gac ccg agg atc tat tcc tgt acc ttc				633
209	Cys Val Gly Thr Leu Gln Tyr Asp Pro Arg Ile Tyr Ser Cys Thr Phe				
210		180	185	190	195
211	acg cag tcc gtc agc tca gcc tac acg atc gcc gtg gtg gtg ttc cat				681
212	Thr Gln Ser Val Ser Ser Ala Tyr Thr Ile Ala Val Val Val Phe His				
213		200	205	210	
214	ttc ata gtt ccg atg ctc gta gtc gtc ttc tgt tac ctg aga atc tgg				729
215	Phe Ile Val Pro Met Leu Val Val Val Phe Cys Tyr Leu Arg Ile Trp				
216		215	220	225	
217	gcc ctg gtt ctt cag gtc aga tgg aag gtg aaa ccg gac aac aaa ccg				777
218	Ala Leu Val Leu Gln Val Arg Trp Lys Val Lys Pro Asp Asn Lys Pro				
219		230	235	240	
220	aaa ctg aag ccc cag gac ttc agg aat ttt gtc acc atg ttt gtg gtt				825
221	Lys Leu Lys Pro Gln Asp Phe Arg Asn Phe Val Thr Met Phe Val Val				
222		245	250	255	
223	ttt gtc ctc ttt gcc att tgc tgg gct cct ctg aac ttc att ggt ctc				873
224	Phe Val Leu Phe Ala Ile Cys Trp Ala Pro Leu Asn Phe Ile Gly Leu				
225		260	265	270	275
226	gtt gtg gcc tcg gac ccc gcc agc atg gca ccc agg atc ccc gag tgg				921
227	Val Val Ala Ser Asp Pro Ala Ser Met Ala Pro Arg Ile Pro Glu Trp				
228		280	285	290	
229	ctg ttt gtg gct agt tac tat atg gca tat ttc aac agc tgc ctc aat				969
230	Leu Phe Val Ala Ser Tyr Tyr Met Ala Tyr Phe Asn Ser Cys Leu Asn				
231		295	300	305	
232	gcg atc ata tat gga cta ctg aac caa aat ttc agg cag gaa tac aga				1017
233	Ala Ile Ile Tyr Gly Leu Leu Asn Gln Asn Phe Arg Gln Glu Tyr Arg				
234		310	315	320	
235	aaa att ata gtc tca ttg tgt acc acc aag atg ttc ttt gtg gat agc				1065
236	Lys Ile Ile Val Ser Leu Cys Thr Thr Lys Met Phe Phe Val Asp Ser				
237		325	330	335	
238	tcc aat cat gta gca gat aga att aaa cgc aaa ccc tct cca tta ata				1113
239	Ser Asn His Val Ala Asp Arg Ile Lys Arg Lys Pro Ser Pro Leu Ile				
240		340	345	350	355
241	gcc aac cat aac cta ata aag gtg gac tcc gtt taa				1149
242	Ala Asn His Asn Leu Ile Lys Val Asp Ser Val				
243		360	365		
244	<210> SEQ ID NO 4				

**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Input Set: I226046.RAW

Line	Error/Warning	Original Text
408	W "N" or "Xaa" used: Feature required	Asn Pro Xaa Xaa Tyr
433	W "N" or "Xaa" used: Feature required	Gly Asn Xaa Phe Val Val
824	W "N" or "Xaa" used: Feature required	Asn Ala Xaa Xaa Tyr